

REMARKS

Claims 1-16 and 25 currently are pending.

Restriction Requirement

The examiner acknowledged the election with traverse of Group I (claims 1-16) but still deemed the requirement proper. Therefore, applicants cancel claims 18-24 which are drawn to an invention nonelected with traverse.

Sequence Disclosure

The examiner has required that the primers located on page 18 of the specification be included in a sequence disclosure. Therefore, applicants submit herein a revised sequence disclosure which includes the primers located on page 18 of the specification.

A copy of the Sequence Listing in computer readable form is attached hereto. The content of the paper copy of the Sequence Listing and the copy of the Sequence Listing in computer readable form is the same, and includes no new matter. It is believed that by submitting the present amendment and sequence listing diskette, the application now fully complies with the requirements of 37 CFR 1.821-1.825. Favorable action by the examiner is solicited.

Foreign Priority

Applicants soon will submit a certified translation of German patent (1970066.9) for proper claiming of priority under 35 USC § 119(a)-(d).

Arrangement of the Specification

As required by the examiner applicants insert proper headings in the specification.

35 USC § 112, first paragraph (Enablement)

The examiner rejected claims 1-16 because the specification while enabling for a DNA sequence encoding a hydroxyphenylpyruvate dioxygenase (HPPD) isolated from barley, an expression vector comprising said isolated DNA sequence, a method of transforming comprising said expression cassette and a plant transformed therewith, does not reasonably provide enablement for other plant DNA sequences encoding an HPPD or uses thereof.

To overcome the rejection applicants amend claim 1 so that it is directed to an isolated DNA sequence encoding a barley HPPD. This amendment is supported by the specification on page 7, line 26. Applicants also add new claim 25, which depends on claim 1.

35 USC § 112, second paragraph (Indefiniteness)

Applicants follow the examiner's suggestions and amend the claims accordingly. Claim 6 has been amended to a process claim which comprises a definite step.

35 USC §102/§ 103

The examiner rejected claim 1 under 35 USC § 102(b) as being anticipated by the intervening reference Krupinska et al. because it discloses SEQ ID NO: 1. Applicants will soon submit a copy of the a translation of the priority application which should overcome this rejection.

Claims 1-13, 5-12, 14 and 16 were rejected under 35 USC § 102(e) as being anticipated by Della Penna et al. (US 6,087,563). Claims 4, 13 and 15 were rejected as being obvious under 35 USC § 103(a) over Della Penna et al. Applicants first point out that claim 1 as amended is not disclosed by Della Penna et al. as this reference does

not disclose a barley HPPD. Furthermore, applicants herein submit a declaration signed by Dr. Jon Falk who has established new data and summarized the already present data. Kindly the consider the arguments in the declaration.

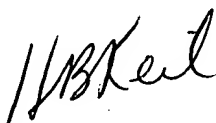
For the reasons expressed above, it is urged that the prior art references cited by the examiner either singly or in combination fail to anticipate or suggest the present invention as defined by the amended claims. Accordingly, a *prima facie* case of obviousness has not been established by the examiner, and the rejection under 35 USC § 103 should be withdrawn.

A check in the amount of \$400.00 is attached to cover the required two month extension of time fee.

Please charge any shortage in fees due in connection with the filing of this paper, including Extension of Time fees to Deposit Account No. 11-0345. Please credit any excess fees to such deposit account.

Respectfully submitted,

KEIL & WEINKAUF



Herbert B. Keil
Reg. No. 18,967

1101 Connecticut Ave., N.W.
Washington, D.C. 20036
(202)659-0100

HBK/DSK/kas

VERSION WITH MARKINGS TO SHOW CHANGES MADE

IN THE CLAIMS:

Cancel claims 18-24.

Amend claims 1-14 and add new claim 25 as follows:

1. (amended) [The] An isolated DNA sequence encoding barley [SEQ ID NO:1 and DNA sequences hybridizing therewith, encoding an] HPPD.

2. (amended) An expression cassette comprising a promoter and [a] the DNA sequence as claimed in claim 1.

3. (amended) An expression cassette as claimed in claim 2, comprising [the] a CaMV 35S promoter.

4. (amended) An expression cassette as claimed in claim 2, comprising [the] a seed-specific phaseolin promoter.

5. (amended) An expression cassette as claimed in claim 2, further comprising the DNA sequence as claimed in claim 1 being functionally linked to another protein in such a way that a joint translation product is formed.

6. (amended) [The use of] A process for transforming plants comprising the step of incorporating into plants the expression cassette as claimed in claim 2 [for transforming plants].

7. (amended) A method of transforming a plant, which comprises introducing [an] the expression cassette as claimed in claim 2 into a plant cell, into callus tissue, into an entire plant or into plant cell protoplasts.

8. (amended) A method of transforming plants, which comprises

1) transferring the expression cassette as claimed in claim 2 into an agrobacterial

strain.

- 2) isolating the recombinant clones formed, and
- 3) [using the latter for transforming plants] transforming a plant with the isolated recombinant clones.

9. (amended) [A] The method as claimed in claim 8, the transformation being accomplished with the aid of the strain *Agrobacterium tumefaciens*.

10. (amended) [A] The method of transforming plants as claimed in claim 7, wherein the transformation is accomplished with the aid of electroporation.

11. (amended) [A] The method of transforming plants as claimed in claim 7, wherein the transformation is accomplished with the aid of the particle bombardment method.

12. (amended) A plant with an elevated vitamin E content, comprising [an] the expression cassette as claimed in claim 2.

13. (amended) [A] The plant as claimed in claim 12, selected from the group consisting of soya, barley, oat[s], wheat, oilseed rape, maize, [or] and sunflower[s].

14. (amended) A method of generating plants with an elevated vitamin E content, which comprises expressing, in plants, [a] the DNA sequence as claimed in claim 1.

25. (new) An isolated DNA sequence as claimed in claim 1, comprising the sequence SEQ ID NO: 1.

COPY OF ALL CLAIMS

1. (amended) An isolated DNA sequence encoding barley HPPD.
2. (amended) An expression cassette comprising a promoter and the DNA sequence as claimed in claim 1.
3. (amended) An expression cassette as claimed in claim 2, comprising a CaMV 35S promoter.
4. (amended) An expression cassette as claimed in claim 2, comprising a seed-specific phaseolin promoter.
5. (amended) An expression cassette as claimed in claim 2, further comprising the DNA sequence as claimed in claim 1 being functionally linked to another protein in such a way that a joint translation product is formed.
6. (amended) A process for transforming plants comprising the step of incorporating into plants the expression cassette as claimed in claim 2.
7. (amended) A method of transforming a plant, which comprises introducing the expression cassette as claimed in claim 2 into a plant cell, into callus tissue, into an entire plant or into plant cell protoplasts.
8. (amended) A method of transforming plants, which comprises
 - 1) transferring the expression cassette as claimed in claim 2 into an agrobacterial strain,
 - 2) isolating the recombinant clones formed, and
 - 3) transforming a plant with the isolated recombinant clones.
9. (amended) The method as claimed in claim 8, the transformation being accomplished with the aid of the strain *Agrobacterium tumefaciens*.

10. (amended) The method of transforming plants as claimed in claim 7, wherein the transformation is accomplished with the aid of electroporation.

11. (amended) The method of transforming plants as claimed in claim 7, wherein the transformation is accomplished with the aid of the particle bombardment method.

12. (amended) A plant with an elevated vitamin E content, comprising the expression cassette as claimed in claim 2.

13. (amended) The plant as claimed in claim 12, selected from the group consisting of soya, barley, oat, wheat, oilseed rape, maize, and sunflower.

14. (amended) A method of generating plants with an elevated vitamin E content, which comprises expressing, in plants, the DNA sequence as claimed in claim 1.

15. A method as claimed in claim 14, wherein the DNA sequence is expressed in a tobacco plant.

16. A method as claimed in claim 14, wherein expression takes place in the leaves or the seeds of the plant.

25. (new) An isolated DNA sequence as claimed in claim 1, comprising the sequence SEQ ID NO: 1.

SEQUENCE LISTING

<110> Seulberger, Harald
 Lerchl, Jenms
 Schmidt, Ralf-Michael
 Krupinska, Karin
 Falk, Jon

<120> DNA sequence encoding a hydroxyphenylpyruvate dioxygenase, and its overproduction in plants

<130> 0050/48141

<140> US 09/462,629

<141> 2000-01-11

<150> PCT/EP98/03832

<151> 1998-06-23

<160> 16

<170> WordPerfect version 6.1

<210> 1

<211> 1565

<212> DNA

<213> hppd from barley

<220>

<221> CDS

<222> 9 ... 1313

<400> 1

cgcacacc atg ccg ccc acc ccc acc acc ccc gcg gct acc ggc gcc gcc 50
 Met Pro Pro Thr Pro Thr Thr Pro Ala Ala Thr Gly Ala Ala
 1 5 10

gcc gcg gtg acg ccg gag cac gcg cga ccg cac cga atg gtc cgc ttc 98
 Ala Ala Val Thr Pro Glu His Ala Arg Pro His Arg Met Val Arg Phe
 15 20 25 30

aac ccg cgc agc gac cgc ttc cac acg ctc tcc ttc cac cac gtc gag 146
 Asn Pro Arg Ser Asp Arg Phe His Thr Leu Ser Phe His His Val Glu
 35 40 45

ttc tgg tgc gcg gac gcc gcc tcc gcc gcc ggc cgc ttc gcg ttc gcg 194
 Phe Trp Cys Ala Asp Ala Ala Ser Ala Ala Gly Arg Phe Ala Phe Ala
 50 55 60

ctc ggc gcg ccg ctc gcc gcc agg tcc gac ctc tcc acg ggg aac tcc 242
 Leu Gly Ala Pro Leu Ala Ala Arg Ser Asp Leu Ser Thr Gly Asn Ser
 65 70 75



gcg cac gcc tcc cag ctg ctc cgc tcg ggc tcc ctc gcc ttc ctc ttc Ala His Ala Ser Gln Leu Leu Arg Ser Gly Ser Leu Ala Phe Leu Phe 80 85 90	290
acc gcg ccc tac gcc aac ggc tgc gac gcc gcc acc gcc tcc ctg ccc Thr Ala Pro Tyr Ala Asn Gly Cys Asp Ala Ala Thr Ala Ser Leu Pro 95 100 105 110	338
tcc ttc tcc gcc gac gcc gcg cgc cgg ttc tcc gcc gac cac ggg atc Ser Phe Ser Ala Asp Ala Ala Arg Arg Phe Ser Ala Asp His Gly Ile 115 120 125	386
gcg gtg cgc tcc gta gcg ctg cgc gtc gca gac gcc gcc gag gcc ttc Ala Val Arg Ser Val Ala Leu Arg Val Ala Asp Ala Ala Glu Ala Phe 130 135 140	434
cgc gcc agt cgt cga cgg ggc gcg cgc ccg gcc ttc gcc ccc gtg gac Arg Ala Ser Arg Arg Arg Gly Ala Arg Pro Ala Phe Ala Pro Val Asp 145 150 155	482
ctc ggc cgc ggc ttc gcg ttc gcg gag gtc gag ctc tac ggc gac gtc Leu Gly Arg Gly Phe Ala Phe Ala Glu Val Glu Leu Tyr Gly Asp Val 160 165 170	530
gtg ctc cgc ttc gtc agc cac ccg gac ggc acg gac gtg ccc ttc ttg Val Leu Arg Phe Val Ser His Pro Asp Gly Thr Asp Val Pro Phe Leu 175 180 185 190	578
ccg ggg ttc gag ggc gta acc aac ccg gac gcc gtg gac tac ggc ctg Pro Gly Phe Glu Gly Val Thr Asn Pro Asp Ala Val Asp Tyr Gly Leu 195 200 205	626
acg cgg ttc gac cac gtc gtc ggc aac gtc ccg gag ctt gcc ccc gcc Thr Arg Phe Asp His Val Val Gly Asn Val Pro Glu Leu Ala Pro Ala 210 215 220	674
gca gcc tac atc gcc ggg ttc acg ggg ttc cac gag ttc gcc gag ttc Ala Ala Tyr Ile Ala Gly Phe Thr Gly Phe His Glu Phe Ala Glu Phe 225 230 235	722
acg gcg gag gac gtg ggc acg acc gag agc ggg ctc aac tcg gtg gtg Thr Ala Glu Asp Val Gly Thr Thr Glu Ser Gly Leu Asn Ser Val Val 240 245 250	770
ctc gcc aac aac tcg gag ggc gtg ctg ctg ccg ctc aac gag ccg gtg Leu Ala Asn Asn Ser Glu Gly Val Leu Leu Pro Leu Asn Glu Pro Val 255 260 265 270	818
cac ggc acc aag cgc cgg agc cag ata cag acg ttc ctg gaa cac cac His Gly Thr Lys Arg Arg Ser Gln Ile Gln Thr Phe Leu Glu His His 275 280 285	866
ggc ggc ccg ggc gtg cag cac atc gcg gtg gcc agc agt gac gtg ctc	914

Gly Gly Pro Gly Val Gln His Ile Ala Val Ala Ser Ser Asp Val Leu	
290 295 300	
agg acg ctc agg aag atg cgt gcg cgc tcc gcc atg ggc ggc ttc gac	962
Arg Thr Leu Arg Lys Met Arg Ala Arg Ser Ala Met Gly Gly Phe Asp	
305 310 315	
ttc ctg cca ccc ccg ctg ccg aag tac tac gaa ggc gtg cga cgc ctt	1010
Phe Leu Pro Pro Pro Leu Pro Lys Tyr Tyr Glu Gly Val Arg Arg Leu	
320 325 330	
gcc ggg gat gtc ctc tcg gag gcg cag atc aag gaa tgc cag gag ctg	1058
Ala Gly Asp Val Leu Ser Glu Ala Gln Ile Lys Glu Cys Gln Glu Leu	
335 340 345 350	
ggg gtg ctc gtc gat agg gac gac caa ggg gtg ttg ctc caa atc ttc	1106
Gly Val Leu Val Asp Arg Asp Asp Gln Gly Val Leu Leu Gln Ile Phe	
355 360 365	
acc aag cca gta ggg gac agg ccg acc ttg ttc ctg gag atg atc cag	1154
Thr Lys Pro Val Gly Asp Arg Pro Thr Leu Phe Leu Glu Met Ile Gln	
370 375 380	
agg atc ggg tgc atg gag aag gac gag aga ggg gaa gag tac cag aag	1202
Arg Ile Gly Cys Met Glu Lys Asp Glu Arg Gly Glu Glu Tyr Gln Lys	
385 390 395	
ggg ggc tgc ggc ggg ttc ggc aaa ggc aac ttc tcc gag ctg ttc aag	1250
Gly Gly Cys Gly Gly Phe Gly Lys Gly Asn Phe Ser Glu Leu Phe Lys	
400 405 410	
tcc att gaa gat tac gag aag tcc ctt gaa gcc aag caa tct gct gca	1298
Ser Ile Glu Asp Tyr Glu Lys Ser Leu Glu Ala Lys Gln Ser Ala Ala	
415 420 425 430	
gtt cag gga tca taggtagaa gctggtcctt gtatcatggt ctcattggagc	1350
Val Gln Gly Ser	
aaaagaaaac aatgttggtt gtaatatgcg tcgcacaatt atatcaatgt tataattggt	1410
gaagctgaag acagatgtat cctatgtatg atgggtgtaa tggatggtag aggggctcac	1470
acatgaagaa aatgtagcgt tgacattggt gtacaatctt gcttgcaagt aaaataaaga	1530
acagattttg agttctgcaa aaaaaaaaaa aaaaa	1565

<210> 2

<211> 434

<212> PRT

<213> hppd from barley

<400> 2

Met Pro Pro Thr Pro Thr Thr Pro Ala Ala Thr Gly Ala Ala Ala Ala
 1 5 10 15
 Val Thr Pro Glu His Ala Arg Pro His Arg Met Val Arg Phe Asn Pro
 20 25 30
 Arg Ser Asp Arg Phe His Thr Leu Ser Phe His His Val Glu Phe Trp
 35 40 45
 Cys Ala Asp Ala Ala Ser Ala Ala Gly Arg Phe Ala Phe Ala Leu Gly
 50 55 60
 Ala Pro Leu Ala Ala Arg Ser Asp Leu Ser Thr Gly Asn Ser Ala His
 65 70 75 80
 Ala Ser Gln Leu Leu Arg Ser Gly Ser Leu Ala Phe Leu Phe Thr Ala
 85 90 95
 Pro Tyr Ala Asn Gly Cys Asp Ala Ala Thr Ala Ser Leu Pro Ser Phe
 100 105 110
 Ser Ala Asp Ala Ala Arg Arg Phe Ser Ala Asp His Gly Ile Ala Val
 115 120 125
 Arg Ser Val Ala Leu Arg Val Ala Asp Ala Ala Glu Ala Phe Arg Ala
 130 135 140
 Ser Arg Arg Arg Gly Ala Arg Pro Ala Phe Ala Pro Val Asp Leu Gly
 145 150 155 160
 Arg Gly Phe Ala Phe Ala Glu Val Glu Leu Tyr Gly Asp Val Val Leu
 165 170 175
 Arg Phe Val Ser His Pro Asp Gly Thr Asp Val Pro Phe Leu Pro Gly
 180 185 190
 Phe Glu Gly Val Thr Asn Pro Asp Ala Val Asp Tyr Gly Leu Thr Arg
 195 200 205
 Phe Asp His Val Val Gly Asn Val Pro Glu Leu Ala Pro Ala Ala Ala
 210 215 220
 Tyr Ile Ala Gly Phe Thr Gly Phe His Glu Phe Ala Glu Phe Thr Ala
 225 230 235 240
 Glu Asp Val Gly Thr Thr Glu Ser Gly Leu Asn Ser Val Val Leu Ala
 245 250 255
 Asn Asn Ser Glu Gly Val Leu Leu Pro Leu Asn Glu Pro Val His Gly
 260 265 270
 Thr Lys Arg Arg Ser Gln Ile Gln Thr Phe Leu Glu His His Gly Gly
 275 280 285

Pro Gly Val Gln His Ile Ala Val Ala Ser Ser Asp Val Leu Arg Thr
 290 295 300

Leu Arg Lys Met Arg Ala Arg Ser Ala Met Gly Gly Phe Asp Phe Leu
 305 310 315 320

Pro Pro Pro Leu Pro Lys Tyr Tyr Glu Gly Val Arg Arg Leu Ala Gly
 325 330 335

Asp Val Leu Ser Glu Ala Gln Ile Lys Glu Cys Gln Glu Leu Gly Val
 340 345 350

Leu Val Asp Arg Asp Asp Gln Gly Val Leu Leu Gln Ile Phe Thr Lys
 355 360 365

Pro Val Gly Asp Arg Pro Thr Leu Phe Leu Glu Met Ile Gln Arg Ile
 370 375 380

Gly Cys Met Glu Lys Asp Glu Arg Gly Glu Glu Tyr Gln Lys Gly Gly
 385 390 395 400

Cys Gly Gly Phe Gly Lys Gly Asn Phe Ser Glu Leu Phe Lys Ser Ile
 405 410 415

Glu Asp Tyr Glu Lys Ser Leu Glu Ala Lys Gln Ser Ala Ala Val Gln
 420 425 430

Gly Ser

<210> 3

<211> 14

<212> DNA

<213> Artificial sequence

<220>

<221> misc_feature

<222> 1.. 14

<223> primer

<400> 3

tttttttttt ttag

14

<210> 4

<211> 14

<212> DNA

<213> Artificial sequence

<220>

<221> misc_feature

<222> 1.. 14

<223> primer

<400> 4

tttttttttt ttca

14

<210> 5

<211> 14

<212> DNA

<213> Artificial sequence

<220>

<221> misc_feature

<222> 1.. 14

<223> primer

<400> 5

tttttttttt ttac

14

<210> 6

<211> 14

<212> DNA

<213> Artificial sequence

<220>

<221> misc_feature

<222> 1.. 14

<223> primer

<400> 6

tttttttttt ttgt

14

<210> 7

<211> 10

<212> DNA

<213> Artificial sequence

<220>

<221> misc_feature

<222> 1.. 10

<223> primer

<400> 7

tacaacgagg

10

<210> 8

<211> 10

<212> DNA

<213> Artificial sequence

<220>
<221> misc_feature
<222> 1.. 10
<223> primer

<400> 8

ggaaccaatc

10

<210> 9
<211> 10
<212> DNA
<213> Artificial sequence

<220>
<221> misc_feature
<222> 1.. 10
<223> primer

<400> 9

aaactccgtc

10

<210> 10
<211> 10
<212> DNA
<213> Artificial sequence

<220>
<221> misc_feature
<222> 1.. 10
<223> primer

<400> 10

tggtaaaggg

10

<210> 11
<211> 10
<212> DNA
<213> Artificial sequence

<220>
<221> misc_feature
<222> 1.. 10
<223> primer

<400> 11

ctgcttgatg

10

<210> 12
<211> 10
<212> DNA
<213> Artificial sequence

<220>
<221> misc_feature
<222> 1.. 10
<223> primer

<400> 12

gttttcgcag

10

<210> 13
<211> 10
<212> DNA
<213> Artificial sequence

<220>
<221> misc_feature
<222> 1.. 10
<223> primer

<400> 13

gatctcagac

10

<210> 14
<211> 10
<212> DNA
<213> Artificial sequence

<220>
<221> misc_feature
<222> 1.. 10
<223> primer

<400> 14

gatctaaccg

10

<210> 15
<211> 10
<212> DNA
<213> Artificial sequence

<220>
<221> misc_feature
<222> 1.. 10

<223> primer

<400> 15

gatcatggtc

10

<210> 16

<211> 10

<212> DNA

<213> Artificial sequence

<220>

<221> misc_feature

<222> 1.. 10

<223> primer

<400> 16

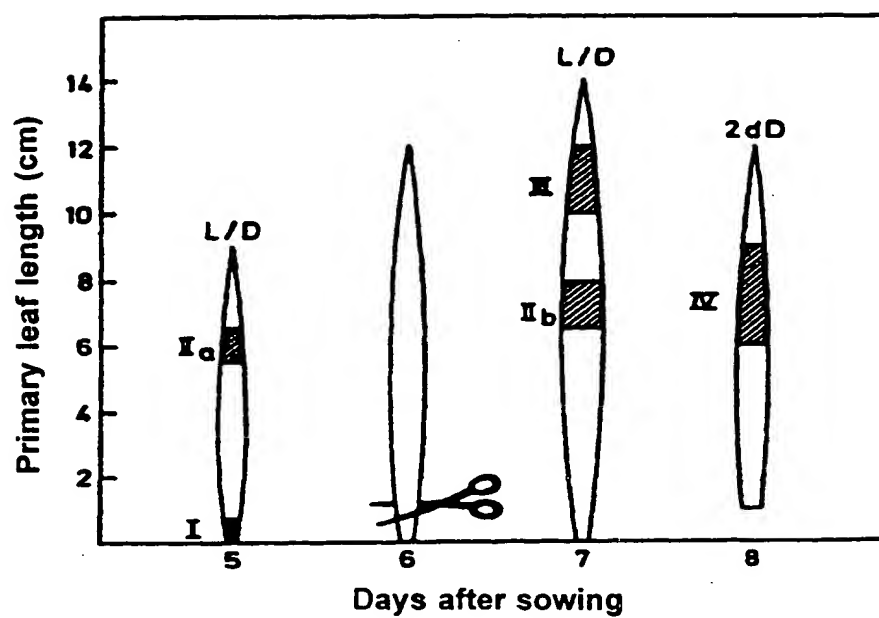
gatctaaggc

10--

(1/7)

FIG. 1

[Fig. 1/7]



[2/7]



FIG. 2

[Fig. 2/7]

I IIa IIb III IV

3100 nt →

1600 nt →



[3/7]

FIG. 3

[Fig. 3/7]

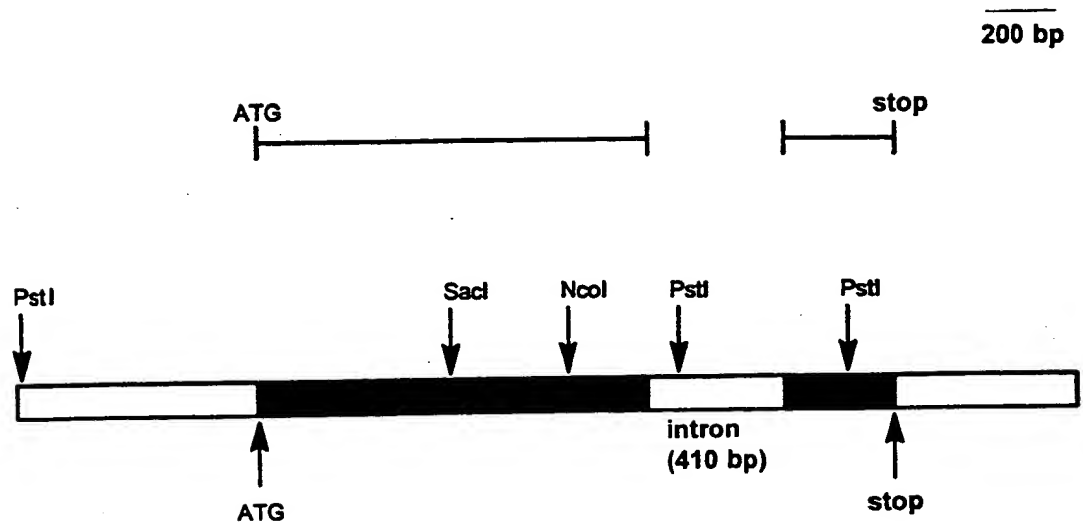


FIG. 4

[Fig. 4/7]

FIG.4A

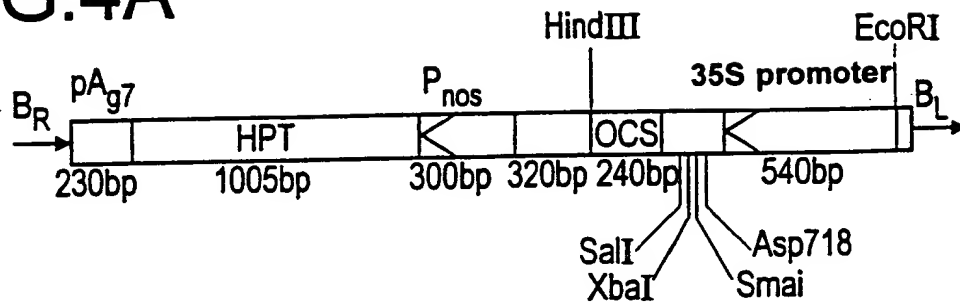
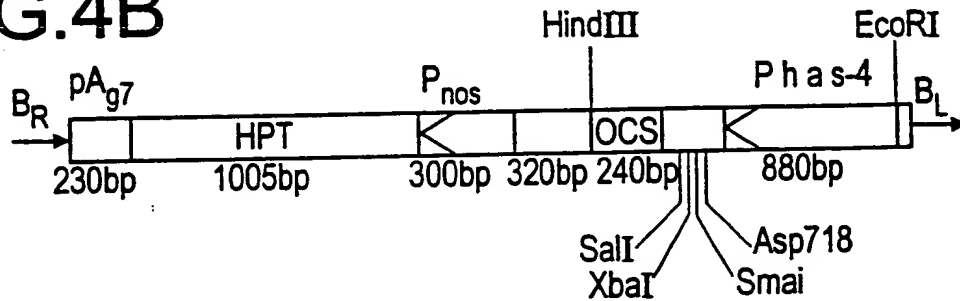


FIG.4B



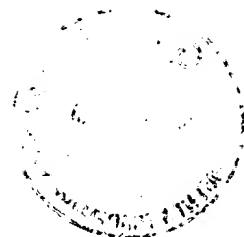


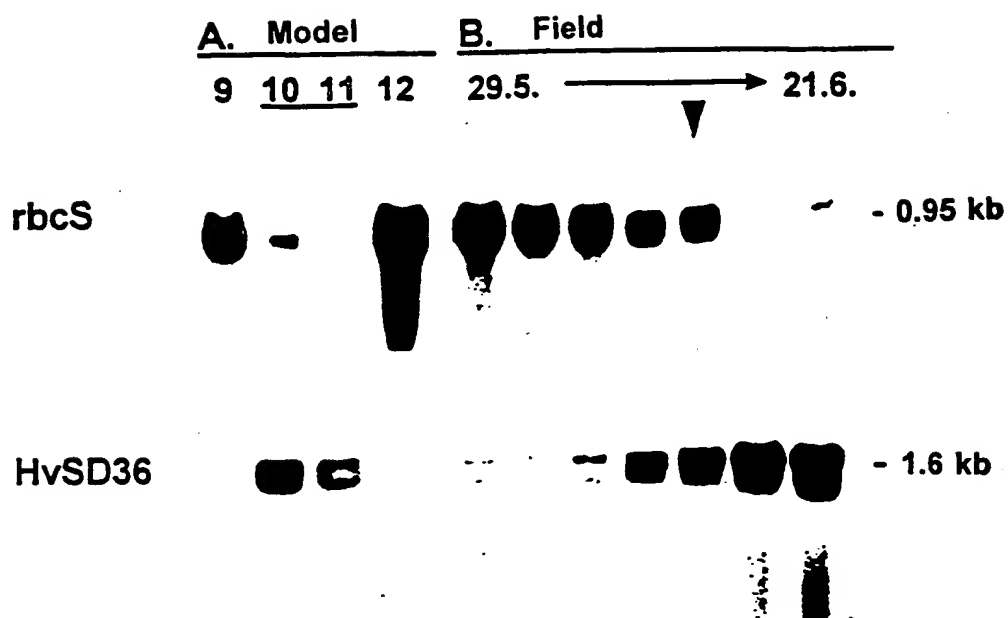
FIG. 5

[Fig. 5/7]



FIG. 6

[Fig. 6/7]



7/7



Fig. 7/7

FIG. 7

B E H X

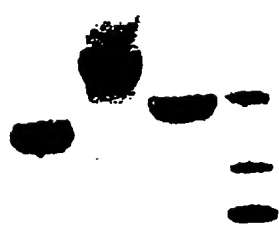


FIG. 8

